Amendments to claims

Claims 15, 18, 20-22, 24, 26-28, and 31-33 have been cancelled without prejudice. Claims 18, 20, 22, 24, 26-28, 31 and 33 relate to non-elected groups.

Claims 16, 17, 19, 23, 25, 29 and 30 have been amended. Support for the amended language is to be found throughout the specification; no new matter has been added. More specifically, support for the language "amino acids 518-533" added to claims 16, 19 and 30 is found in the specification on page 3, line 18. Support for the language "amino acids 551-565" added to claim 16 is found in the specification on page 3, line 22. Support for the language "or a variant thereof" added to claims 16, 19 and 30 is found in the specification on page 7, lines 13 and 14. Support for the language "characterized in that an antigen in said mixture is bound to a label which generates a detectable signal when said antigen is bound to said antibody" and "detecting the signal generated as a measure of said HIV antibody in the sample" added to claims 16 and 29 is found in the specification on page 2, line 17, and page 5, lines 9 and 10.

Rejection under 35 USC §112, second paragraph

The examiner has rejected claims 15-17, 19, 21, 23, 25, 29, 30 and 32 under 35 USC §112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicants regards as their invention.

Claims 15-16, 19, 29 and 30 are rejected for being vague and indefinite in that the metes and bounds of the antigen are not defined. The examiner argues that it is known that gp41 is the transmembrane domain of the HIV1 envelope protein that is about 350 amino acids long; however, not all the regions of the 350 amino acid sequence encode the antigenic peptide and can be utilized to detect the antibody against gp41. The examiner further argues that the claims should point out precisely which part of the sequence of HIV1 gp41 is intended.

By way of the present amendment, Applicants have cancelled claim 15 and have amended claim 16 to recite the definitions of the relevant sequences as taught in the specification on page 3, lines 18 and 22, as being from epitope region II, amino acids 518-533 of the Consensus D sequence or a variant thereof (as taught on page 8, Table 1) and epitope region I, amino acids 551-565 of the Consensus E sequence or a variant thereof (as taught on pages 8-9, Table 2), respectively. The examiner's reconsideration of the rejection is respectfully requested.

Claims 15 and 16 are rejected as being vague in the recitation of the relative term "derived". In response, claim 16, as well as claims 19, 25 and 30, have now been amended, and use of the term "derived" has been avoided. The examiner's reconsideration of the rejection is respectfully requested.

Claim 16 has been rejected as being vague and indefinite in the recitation of "corresponding region." In response, claim 16 has now been amended, and the term "corresponding region" has been replaced by the definite language "epitope II region" and "epitope I region". The examiner's reconsideration of the rejection is respectfully requested.

Claims 16, 19, 21 and 25 are rejected as being vague and indefinite in that the metes and bounds of the epitope regions are not defined. The examiner argues that the claims should point out what are the exact sequence structures defined for the regions in the claims. Applicants have amended claims 16 and 19 to now recite the specific epitope regions I and II as taught in the specification on page 3, lines 18 and 22.

Claim 21 has been rejected as being vague and indefinite in that the metes and bounds of the consensus sequence is not defined. Applicants have cancelled claim 21, making the rejection moot.

Claims 17 and 23 are rejected as being vague and indefinite in that the metes and bounds of the partial sequences thereof are not defined. The examiner argues that the term

"partial" in both claims is relative and can be defined by the claims, but the specification does not provide a standard for ascertaining the requisite degree. Applicants have amended claims 17 and 23 so that the sequences SEQ ID NOs 1 to 11 are now recited specifically. Reconsideration of the rejection by the examiner is requested.

Claims 15-16 and 29 are rejected as being incomplete for omitting essential steps. The examiner argues that the omitted steps are detecting the binding signal of said HIV antigen bound to the suspected antibody etc.

In response, Applicants have now amended claims 16 and 29 to recite the step of detecting the signal generated by a label as a measure of HIV antibody in the sample. Reconsideration of the rejection is requested.

In light of the above comments and amendments, the Examiner's reconsideration of his rejection of claims 15-17, 19, 21, 23, 25, 29, 30 and 32 under 35 USC §112, second paragraph, is respectfully requested by Applicants.

Rejection under 35 USC §112, first paragraph

The examiner has rejected claims 15-17, 19, 21, 23, 25, 29, 30 and 32 under 35 USC §112, first paragraph, because the specification, while being enabled for detecting the anti-gp41 antibody of HIV1 group M by using a mixture of two sequences selected from SEQ IDs NO 1-11 as an antigen peptide, does not reasonably provide enablement for using any or all sequences encoding the epitope 1 and II in any kind of mixture or length for detecting the antibody against gp41 of HIV group M. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the invention commensurate in scope with these claims. The examiner argues that the scope of the claims read on an immunoassay method for detecting any or all antibodies against gp41 from different subtypes of HIV1 group M with any or all kinds of the mixture of the antigen from the epitope regions II and I of the consensus sequence of HIV1-subtype D and subtype O.

Applicants have now amended claims 16, 19 and 30 to recite specifically the amino acid regions for epitopes I and II, and the examiner's reconsideration of the rejection is respectfully requested.

Rejection under 35 USC §103(a)

The examiner has rejected claims 15-17, 19, 21, 23, 25, 29, 30 and 32 under 35 USC §103 (a) as being unpatentable over De Ley *et al.*, WO 93/18054 (hereinafter "De Ley"), and Chamaret *et al.*, FR 2730493 A1 (hereinafter "Chamaret"). The examiner argues that Chamaret teaches using a 34 amino acid polypeptide of gp41 derived from the HIV1 group M subtype D and has 100% homology to SEQ ID NO. 6, which can be used for detecting HIV1 gp41 antibody by an immunoassay method. Chamaret does not teach using a mixture of peptide antigens for detecting variable antibodies against gp41 from different subtypes of HIV1 group M. The examiner argues further that De Leys teaches a method for using a mixture of biotinylated peptides for detecting an antibody against HIV1 gp 41 wherein one of the biotinylated peptide antigens has 100% homology to SEQ ID NO. 3 of the current application, wherein the length of the peptide can be more preferably from 4-25 amino acids. Therefore, the examiner argues, it would have been obvious to one of ordinary skill in the art to be motivated by Chamaret and DeLeys to reduce the length of the antigen peptide disclosed in the cited references to the range of 4 to 25 and further use the method taught by De Leys to mix the biotinylated peptides for detecting variable antibodies against the transmembrane domain of the envelope protein gp41 of HIV1 different subtype infection without unexpected results. Hence the claimed invention as a whole is *prima facie* obvious absent unexpected results.

Applicants traverse the rejection. According to the examiner, Charmaret discloses the use of an antigen of HIV1 group M subtype D, corresponding to Applicants' SEQ. ID NO. 6. De Leys teaches using a peptide corresponding to Applicants' SEQ. ID No. 3, which is also HIV1 group M subtype D. The combination of Charmaret with De Leys would lead to an assay with two antigens both of HIV1 group M subtype D, which is not

what Applicants are claiming. Applicants claim the combination of a group D with a group M (not D) peptide. This combination is neither taught nor suggested in De Leys nor in Charmaret nor in the combination of De Leys and Charmaret together. The combination of De Leys and Charmaret do not give Applicants' invention. Applicants argue that the examiner has failed to make a *prima facie* case of obviousness, and reconsideration of his rejection of the claims is respectfully requested.

* * * * * *

Applicants submit that their application is now in condition for allowance, and favorable reconsideration of their application in light of the above amendments and remarks is respectfully requested. Allowance of claims 16, 17, 19, 23, 25, 29, 30 and 32 at an early date is earnestly solicited.

The Examiner is hereby authorized to charge any fees associated with this Amendment to Deposit Account No. 50-0877. A duplicate copy of this sheet is enclosed.

Respectfully submitted,

September 27, 2001

Marilyn L. Amick, Reg. No. 30,444
Roche Diagnostics Corporation
9115 Hague Road
Indianapolis, IN 46250-0457
Phone: 317-521-7561
Fax: 317-521-2883

16. An immunoassay method for detection of an antibody against HIV comprising:

a. providing a sample suspected of containing an antibody against HIV,

b. contacting said sample with at least one antigen mixture selected from the group consisting of a mixture of an antigen from the epitope region II, amino acids 518-533, of the Consensus sequence of an HIV1-subtype D isolate or a variant thereof and an antigen from the epitope II region of gp41 of a different HIV1 subtype of the M group and a mixture of an antigen from epitope region I, amino acids 551-565, of the Consensus sequence of an HIV1-subtype E isolate or a variant thereof and an antigen derived from the epitope region I of gp41 of a different HIV1 subtype of the M group, characterized in that an antigen in said mixture is bound to a label which generates a detectable signal when said antigen is bound to said antibody, and

c. detecting the signal generated as a measure of said HIV antibody in the sample.

17. The method of claim 16 wherein said antigen of an HIV1-subtype D isolate corresponds to a sequence selected from the group consisting of SEQ ID NOs. 1 to 11.

19. An antigen mixture comprising an antigen from the epitope region II, amino acids 518-533, of the consensus sequence of an HIV1-subtype D isolate or a variant thereof and an antigen from the epitope II region of gp41 of a different HIV1 subtype of the group M.

23. The antigen mixture of claim 19 wherein said antigen of an HIV1-subtype D isolate corresponds to a sequence selected from the group consisting of SEQ ID NOs. 1 to 11.

25. The antigen mixture of claim 19, further comprising an antigen from epitope region I or II of HIV1-subtype O.

29. An immunoassay method for detection of an antibody against HIV comprising:

a. providing a sample suspected of containing an antibody against HIV,

b. contacting said sample with an antigen comprising a sequence selected from the group consisting of SEQ ID NOs. 1 to 11, said sequence having a minimum length of 7 amino acids, characterized in that said antigen is bound to a label which generates a detectable signal when the antigen is bound to said antibody, and

c. detecting the signal generated as a measure of said HIV antibody in the sample.

30. A reagent for the detection of an antibody against HIV by means of an immunoassay comprising an antigen mixture comprising an antigen from the epitope region II, amino acids 518-533, of the consensus sequence of an HIV1-subtype D isolate or a variant thereof and an antigen from the epitope II region of gp41 of a different HIV1 subtype of the group M.